FIGURE 1

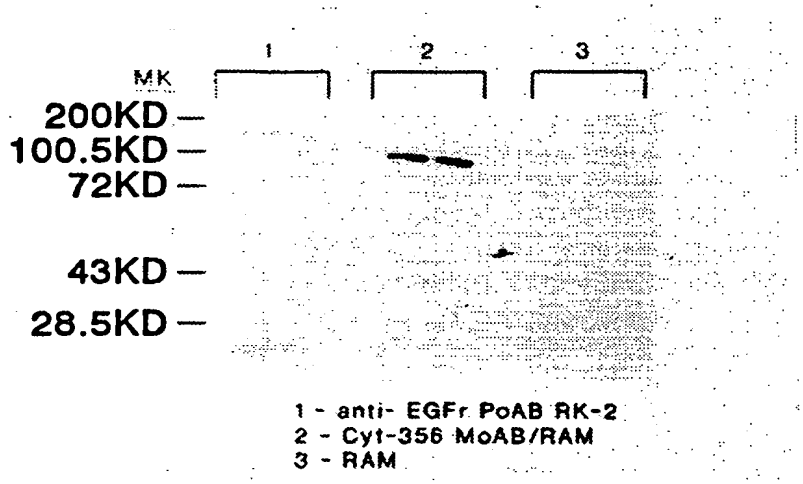
MK
1
2
3
200KD
100.5KD
72KD
43KD
28.5KD
1 - anti- EGFr PoAB RK-2
2 - Cyt-356 MoAB/RAM
3 - RAM

FIGURE 2A

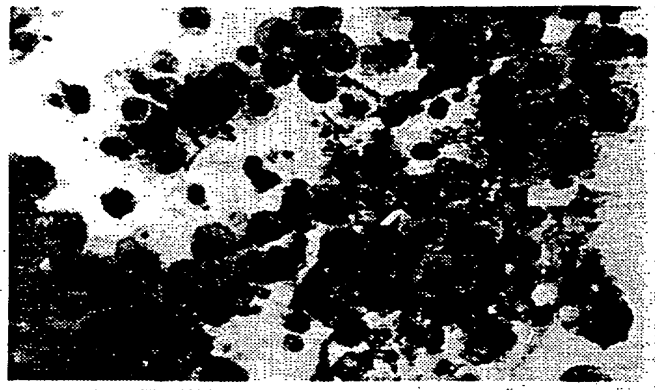

FIGURE 2B

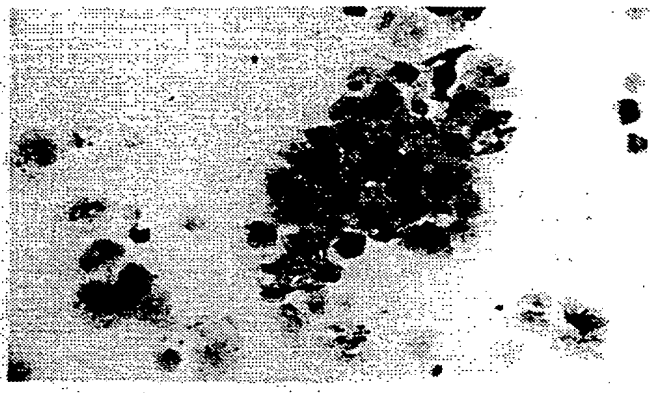

FIGURE 2C

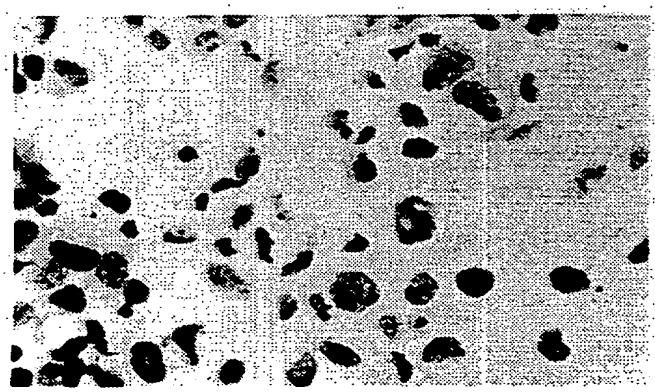

FIGURE 2D

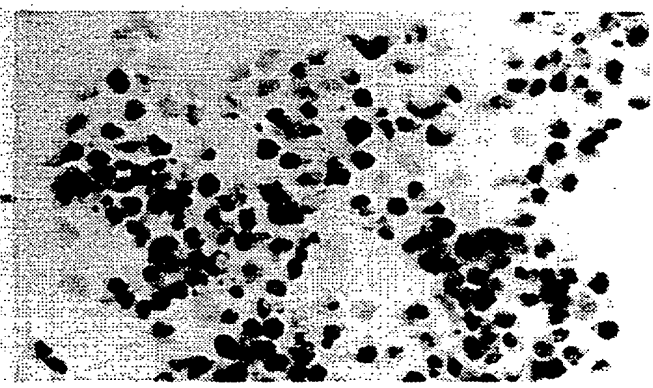

FIGURE 3A

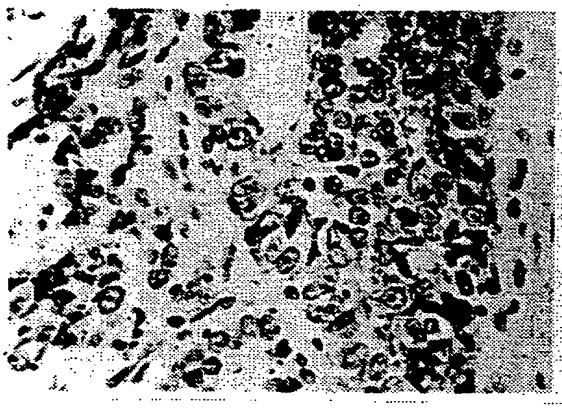

FIGURE 3B

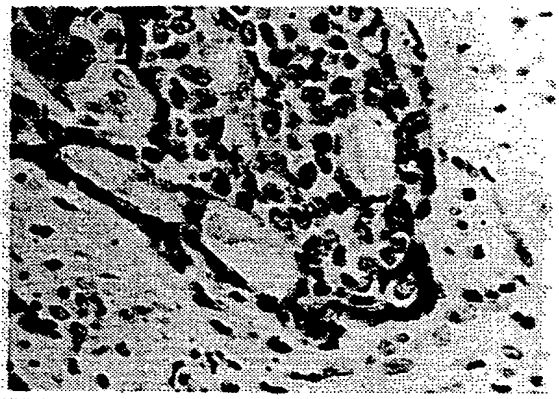

FIGURE 3C

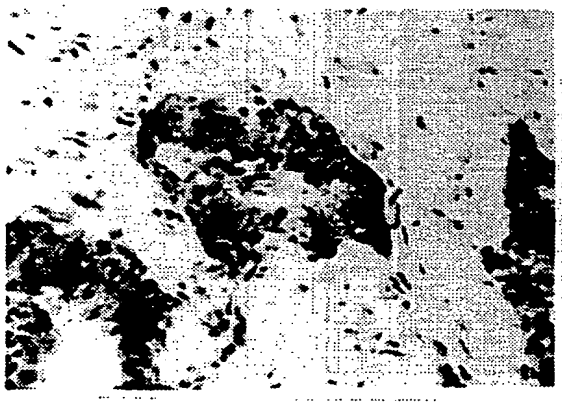

FIGURE 3D

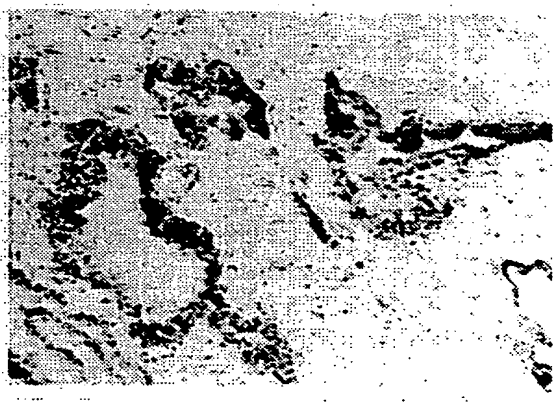

FIGURE 4

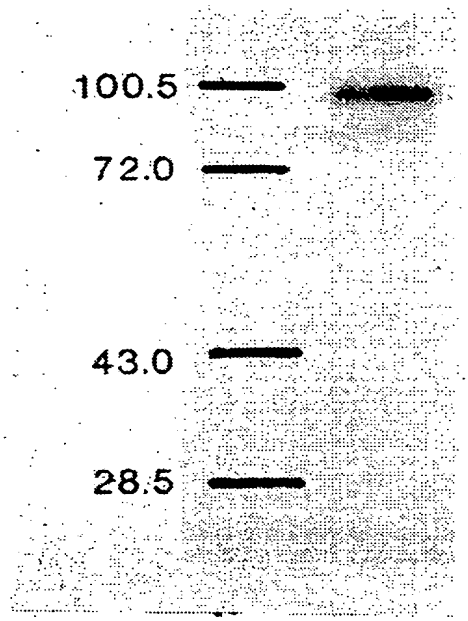

FIGURE 5

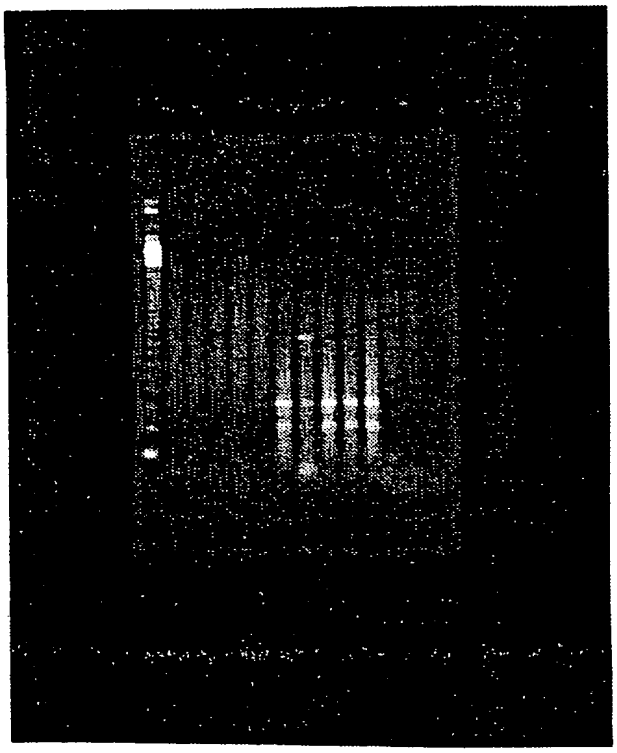

FIGURE 6A FIGURE 6B

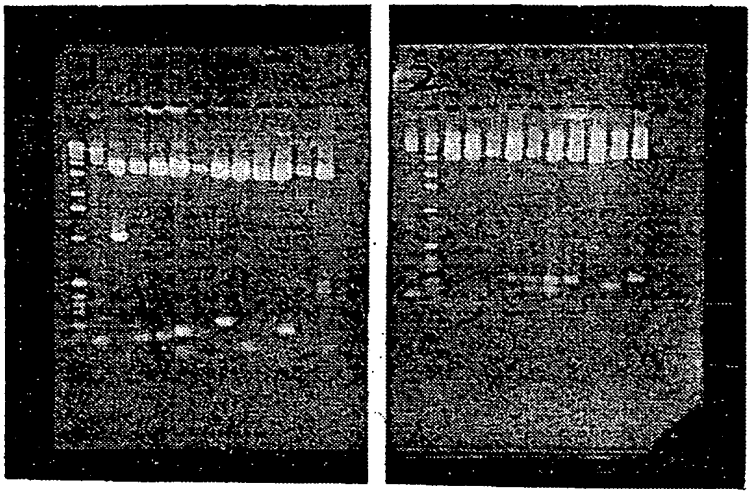

FIGURE 7

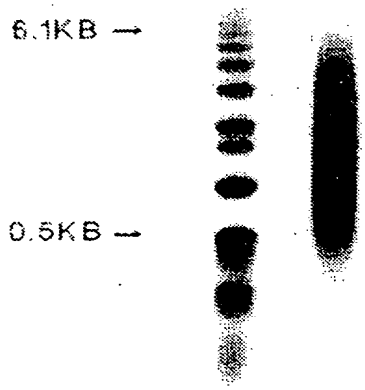

FIGURE 8

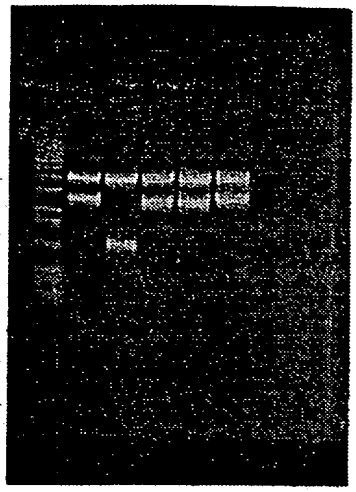

FIGURE 9

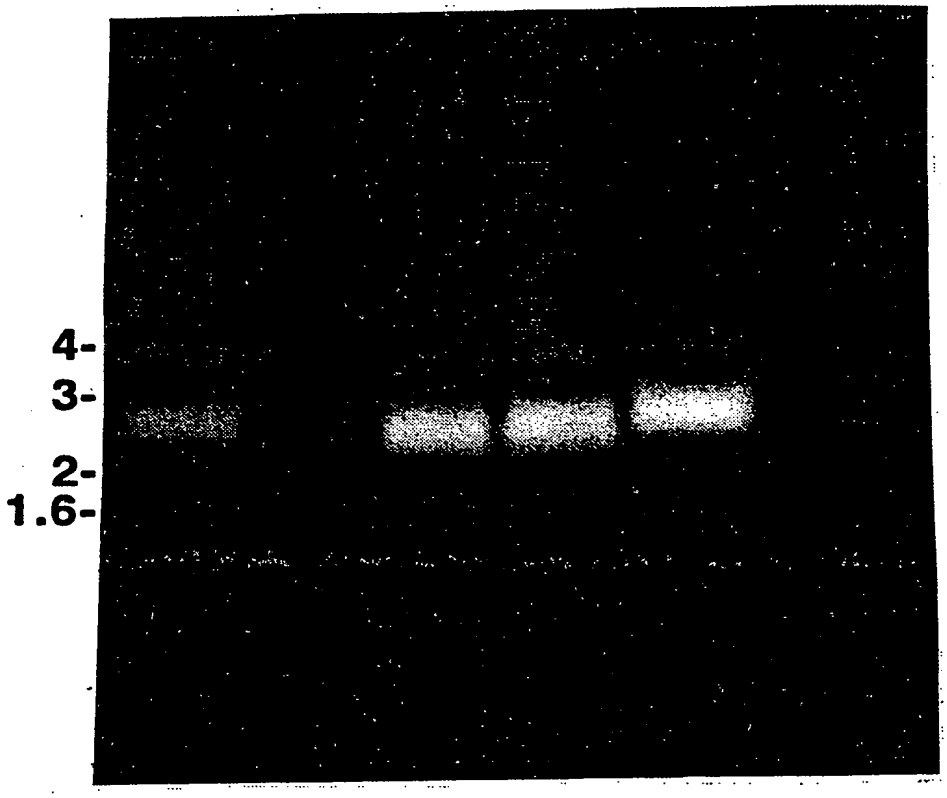

FIGURE 10

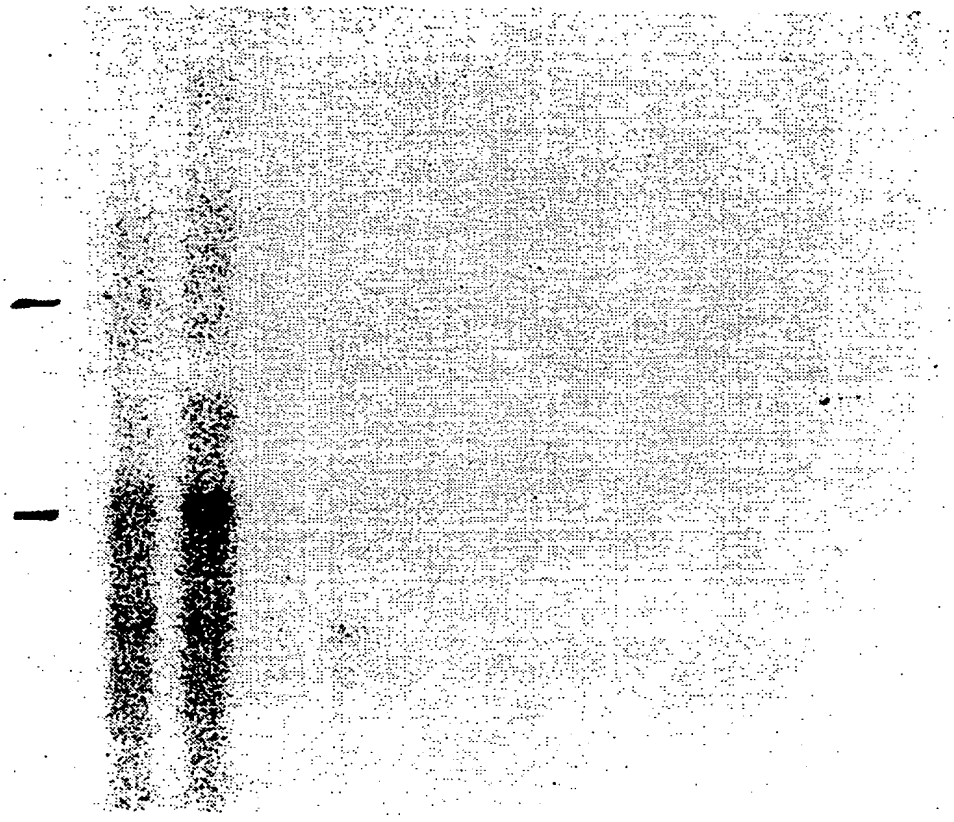

FIGURE 11

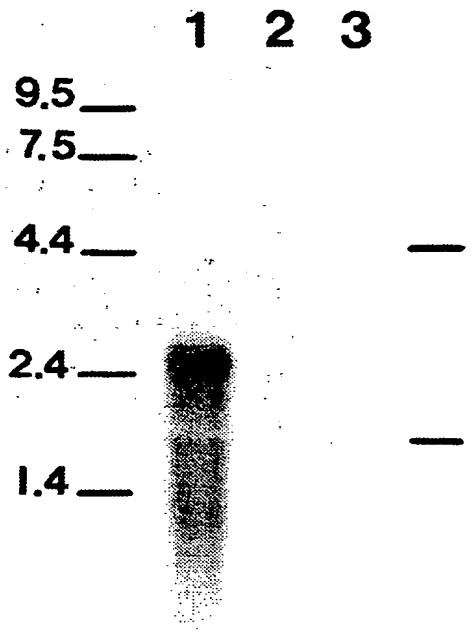

FIGURE 12A

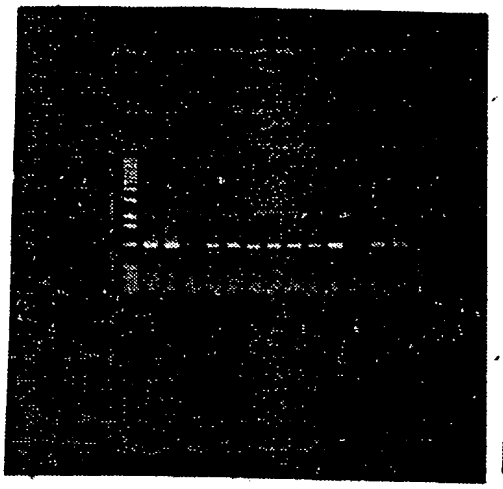

FIGURE 12B

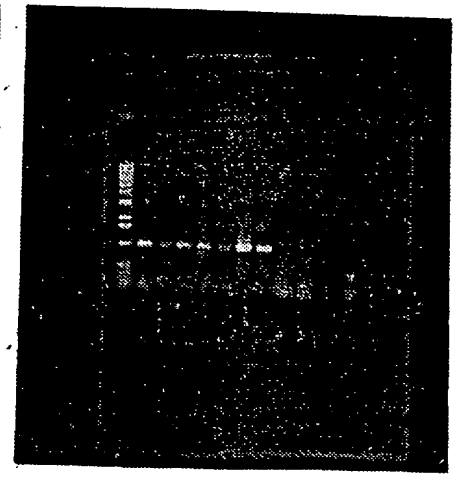

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FIGURE 13

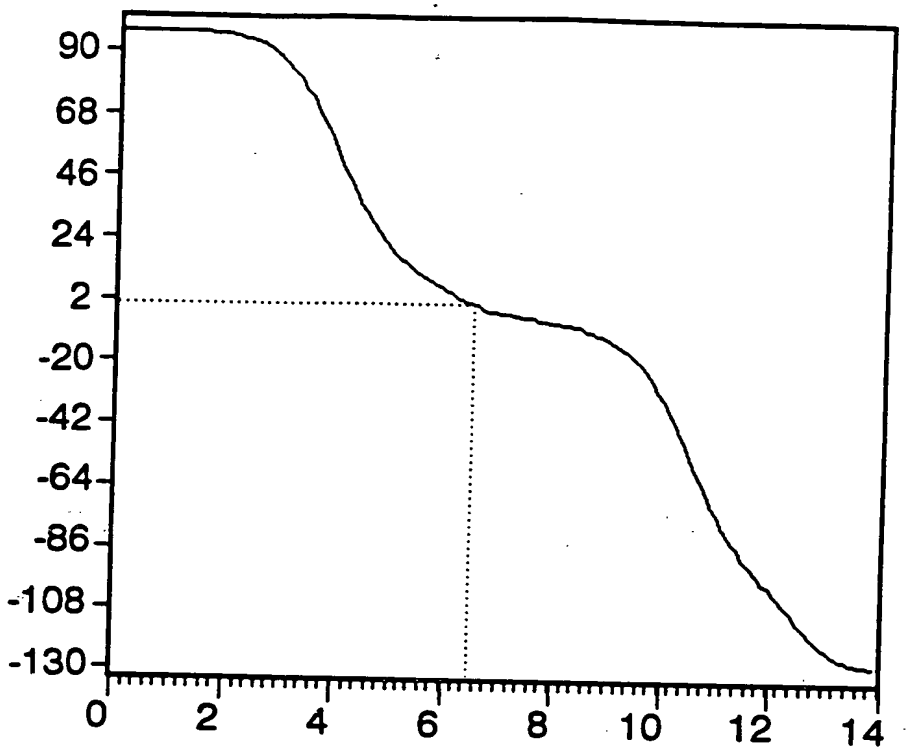


FIGURE 14-1

Done on sequence PMSANTIGEN.
Total number of residues is: 750.
Analysis done on the complete sequence.

In Helical	(H) conformation	[DC =	-75 CNAT] :	264 AA =>	35.2%
In Extended	(E) conformation	[DC =	-88 CNAT] :	309 AA =>	41.2%
In Turn	(T) conformation	[DC =	0 CNAT] :	76 AA =>	10.1%
In Coil	(C) conformation	[DC =	0 CNAT] :	101 AA =>	13.4%

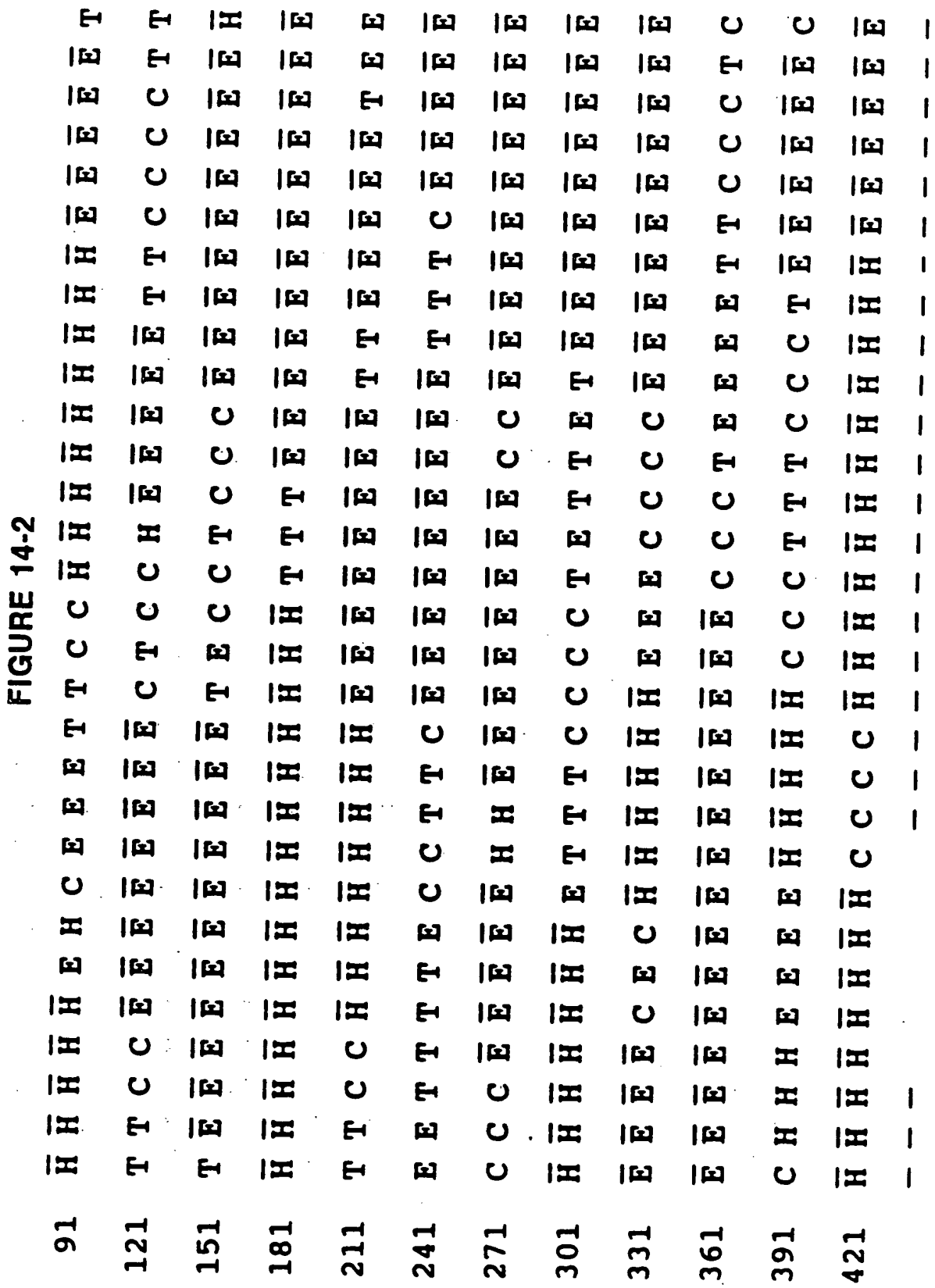
Sequence shown with conformation codes.
==========

Consecutive stretch of 5 or more residues in a given conformation are overlined.

1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	E	E	E	T	T	E	E	E	E	E	E	E	E	E	E
31	E	E	E	E	E	E	H	H	H	H	H	H	C	C	C	C	C	C	T	H	H	H	H	H	H	H	H	H	H
61	H	H	H	H	H	H	H	H	H	H	H	H	E	E	E	T	T	E	E	E	E	C	C	C	C	C	H	H	H	H

1066381

FIGURE 14-2



08/466381

FIGURE 14-3

451 E E E C C E E T T E E E E E E E E E E E E E H H H H H H H H

481 H̅ C C H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ T T T C̅ C̅ C̅ C̅ C̅ T E̅ E̅ E̅ E̅ E̅

511 E̅ E̅ E̅ E̅ E̅ C̅ C̅ C̅ C̅ C̅ E E E H̅ H̅ H̅ H̅ H̅ T C C C E E E T T E C T

541 T E T̅ T̅ T̅ T̅ T̅ C E̅ E̅ E̅ E̅ E̅ E̅ E̅ E̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅

571 H̅ H̅ H̅ H̅ E H E̅ E̅ E̅ E̅ E̅ E̅ E̅ E̅ E̅ H̅ H̅ H̅ H̅ H̅ E̅ E̅ E̅ E̅ E̅ E̅ T H̅ H̅ H̅

601 H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ E̅ E̅ E̅ E̅ E̅ H C C H̅ H̅ H̅ H̅ H̅ E̅ E̅ E̅ E̅ E̅ E̅ E̅

631 H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ T T T C C E̅ E̅ E̅

661 E̅ E̅ E̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ E E T T C C C T E̅ E̅ E̅ E̅ E̅ E̅ E̅

691 E̅ E̅ E̅ E̅ T C C C C T E̅ E̅ E̅ E̅ E̅ E̅ T E E H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ C C

721 C H̅ H̅ H̅ H̅ H̅ H̅ H̅ E̅ E̅ E̅ E̅ E̅ E̅ E̅ E̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅ H̅

FIGURE 14-4

```
Semi-graphical output.
======================

Symbols used in the semi-graphical representation:

Helical  conformation: X      Extended conformation: -
  Turn   conformation: >        Coil   conformation: *

        10        20        30        40        50
        |         |         |         |         |
MWNLLHETDSAVATARRPRWLCAGALVLAGGFFLLGFLFGWFIKSSNEAT
XXXXXXXXXXXXXX--->>----------------------XXXXXX******>X
XXXXXXXXXXXXXX--->>----------------------XXXXXX******>X

        60        70        80        90        100
        |         |         |         |         |
NITPKHNMKAFLDELKAENIKKFLYNFTQIPHLAGTEQNFQLAKQIQSQW
```

FIGURE 14-5

```
XXXXXXXXXXXXXXXXXXXX---->----*****XXXXXXXXX-X*--
XXXXXXXXXXXXXXXXXXXX---->----*****XXXXXXXXX-X*--

      110       120       130       140       150
       |         |         |         |         |
KEFGLDSVELAHYDVLLSYPNKTHPNYISIINEDGNEIFNTSLFEPPPPG

-><***XXXXXXXXX----><><**----------*><**X----><*****><
-><***XXXXXXXXX----><><**----------*><**X----><*****><

      160       170       180       190       200
       |         |         |         |         |
YENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINCSGKI
```

FIGURE 14-6

```
>----------->-**>***----------XXXXXXXXXXXXXXXX>>>--
>----------->-**>***----------XXXXXXXXXXXXXXXX>>>--

      210       220       230       240       250
       |         |         |         |         |
VIARYGKVFRGNKVKNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNLPG

----------->>**XXXXXXXX----------->----->>>>-**>
----------->>**XXXXXXXX----------->----->>>>-**>

      260       270       280       290       300
       |         |         |         |         |
GGVQRGNILNLNGAGDPLTPGYPANEYAYRRGIAEAVGLPSIPVHPIGYY

>*----------->>>*----***-----XX----------**----------
>*----------->>>*----***-----XX----------**----------

      310       320       330       340       350
       |         |         |         |         |
DAQKLLEKMGGSAPPDSSWRGSLKVPYNVGPGFTGNFSTQKVKMHIHSTN

XXXXXX->>>>****>->>->----------*-*XXXXX--****
XXXXXX->>>>****>->>->----------*-*XXXXX--****

      360       370       380       390       400
       |         |         |         |         |
EVTRIYNVIGTLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHEIVR
```

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FIGURE 14-7

```
-------------------------***>---->>***>**XXX----XX
-------------------------***>---->>***>**XXX----XX

       410       420       430       440       450
         |         |         |         |         |
SFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEWAEENSRLLQERGVAYI

XXX***>>>***>------*XXXXXXXX****XXXXXXXXXXXX------
XXX***>>>***>------*XXXXXXXX****XXXXXXXXXXXX------

       460       470       480       490       500
         |         |         |         |         |
NADSSIEGNYTLRVDCTPLMYSLVHNLTKELKSPDEGFEGKSLYESWTKK

---**-->>-------------XXXXXXXXX**XXXXXXXXXXXXX>>>*
---**-->>-------------XXXXXXXXX**XXXXXXXXXXXXX>>>*

       510       520       530       540       550
         |         |         |         |         |
SPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYP

****>----------*****---XXXXX>***--->>-*>>->>>>>*--
****>----------*****---XXXXX>***--->>-*>>->>>>>*--

       560       570       580       590       600
         |         |         |         |         |
```

FIGURE 14-8

```
LYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDY

------XXXXXXXXXXXXXXXX-X----------XXXXX---------->XXX
-----XXXXXXXXXXXXXXXXX-X----------XXXXX---------->XXX

      610       620       630       640       650
       |         |         |         |         |
AVVLRKYADKIYSISMKHPQEMKTYSVSFDSLFSAVKNFTEIASKFSERL

XXXXXXXXXX-----X**XXXXX----------XXXXXXXXXXXXXXXXXX
XXXXXXXXXX-----X**XXXXX----------XXXXXXXXXXXXXXXXXX

      660       670       680       690       700
       |         |         |         |         |
QDFDKSNPIVLRMMNDQLMCLERAFIDPLGLPDRPFYRHVIYAPSSHNKY

XX>>>**----------XXXXXXXXXXX-->>***>----------->*****>
XX>>>**----------XXXXXXXXXXX-->>***>----------->*****>

      710       720       730       740       750
       |         |         |         |         |
AGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAETLSEVA

------>--XXXXXXXXX***XXXXXXXX----------XXXXXXXXXXXX
------>--XXXXXXXXX***XXXXXXXX----------XXXXXXXXXXXX
```

FIGURE 15A

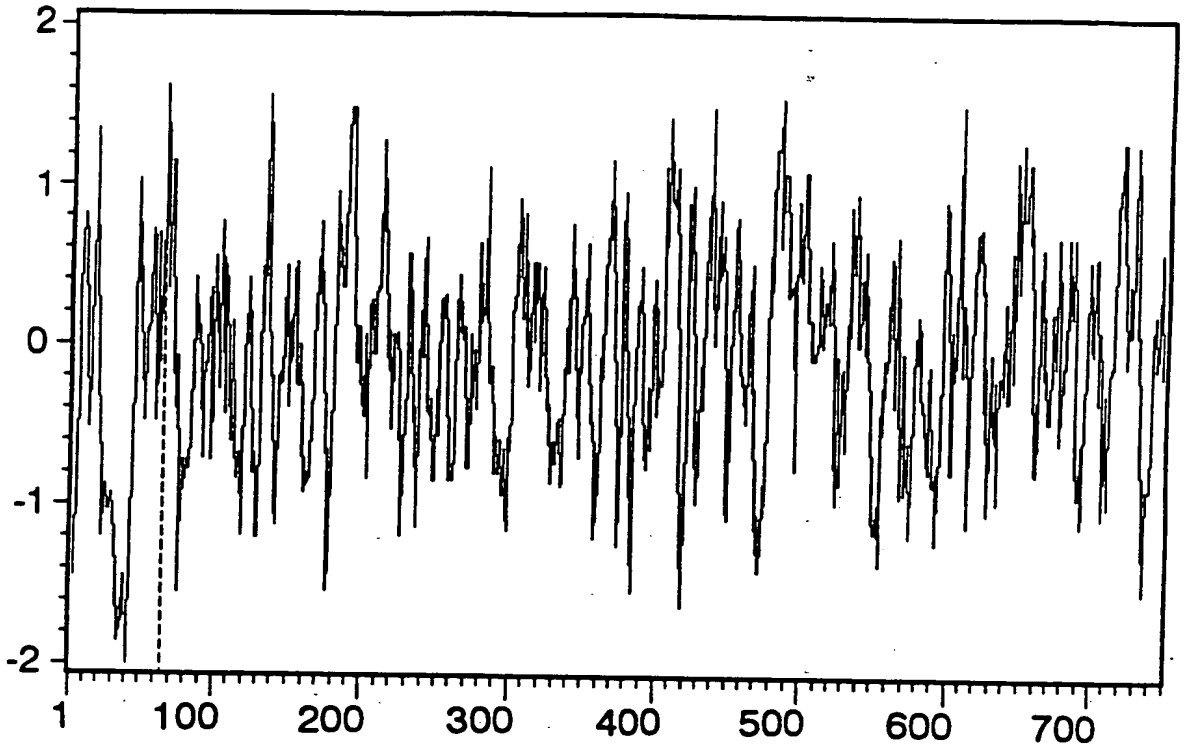


FIGURE 15B

```
**********************************************
* PREDICTION OF ANTIGENIC DETERMINANTS *
**********************************************

Done on sequence PMSANTIGEN.
Total number of residues is: 750.
Analysis done on the complete sequence.

The method used is that of Hopp and Woods.
The averaging group length is: 6 amino acids.
-> This is the value recommended by the authors <-

-----------------------------------------

The three highest points of hydrophilicity are:

( 1)  Ah= 1.62 : From   63 to   68 : Asp-Glu-Leu-Lys-Ala-Glu
( 2)  Ah= 1.57 : From  132 to  137 : Asn-Glu-Asp-Gly-Asn-Glu
( 3)  Ah= 1.55 : From  482 to  487 : Lys-Ser-Pro-Asp-Glu-Gly

Ah stands for: Average hydrophilicity.

Note that, on a group of control proteins, only the highest point was in 100
of the cases assigned to a known antigenic group. The second and third point
gave a proportion of 33% of incorrect predictions.
```


PCT/US93/10381

FIGURE 16-1

```
The best scores are:                                          initn  init1   opt
CHKTFER   G.gallus mRNA for transferrin receptor               203    120    321
RATTRFR   Rat transferrin receptor mRNA, 3' end.               164    164    311
HUMTFRR   Human transferrin receptor mRNA, complete cd         145    145    266


CHKTFER   G.gallus mRNA for transferrin receptor               203  120  321
  51.9% identity in 717 nt overlap

       1020       1030       1040       1050       1060       1070
pmsgen TGTCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACCAGGTTA
                                        :::  : :::::::::  ::: :::::  :
CHKTFE TACACTTATCCCATTCGGACATGCCCACCTTGGAACTGGAGACCCTTACACCCCAGGCTT
           990       1000       1010       1020       1030       1040

       1080       1090       1100       1110       1120       1130
pmsgen CCCAGCAAATGAATATGCTTATAGGCGTGGAATTGCAGAGGCTGTTGGTCTTCCAAGTAT
       :::  :     :  :  :  :   :  :  :   :  ::  ::   :: :: ::     ::
CHKTFE CCCTTCGTTCAACCACACCCA---GTTTCCACCAGTTGAATCTTCAGGACTACCCCACAT
          1050       1060          1070       1080       1090       1100

       1140       1150       1160       1170       1180       1190
pmsgen TCCTGTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTC
       : :::::::  : ::       :  ::  :::   : :::  :    ::::::: :::
CHKTFE TGCTGTTCAGACCATCTCTAGCAGTGCAGCAGCCAGGCTGTTCAGCAAAATGGATGGAGA
             1110       1120       1130       1140       1150       1160
```

FIGURE 16-2

```
          1200       1210       1220       1230       1240       1250
pmsgen AGCACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGG
         ::    : :: ::  : :::: :::     :: :     :::  :: ::  :::
CHKTFE CACATGCTCTGA-AG--GTTGGAAAGGTGCGATCCA---TTCCTGTAAGGT--GAC--AA
            1170       1180       1190       1200            1210

          1260       1270       1280       1290       1300       1310
pmsgen CTTTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGT
         :    : ::: :     : : :  :: :: ::  :  :  :  ::  : :::   :::
CHKTFE CAAAGCAGGAGA----GCCAGA-TAATGGTGAAACTAGATGTGAACAATTCCATGAAAGA
            1220            1230       1240       1250       1260

          1320       1330       1340       1350       1360       1370
pmsgen GACAAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGATATGT
         :  :  :::   ::  :  : ::: :: ::   :::   :  ::::: ::  : :::::
CHKTFE CAGGAAGATTCTGAACATCTTCGGTGCTATCCAGGGATTTGAAGAACCTGATCGGTATGT
          1270       1280       1290       1300       1310       1320

          1380       1390       1400       1410       1420       1430
pmsgen CATTCTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGC
         :  : ::::  ::  : :::::: ::::     :: :    : :  ::   : :::: :
CHKTFE TGTGATTGGAGCCCAGAGAGACTCCTGGGGCCCAGGAGTGGCTAAAGCTGGCACTGGAAC
          1330       1340       1350       1360       1370       1380
```

FIGURE 16-3

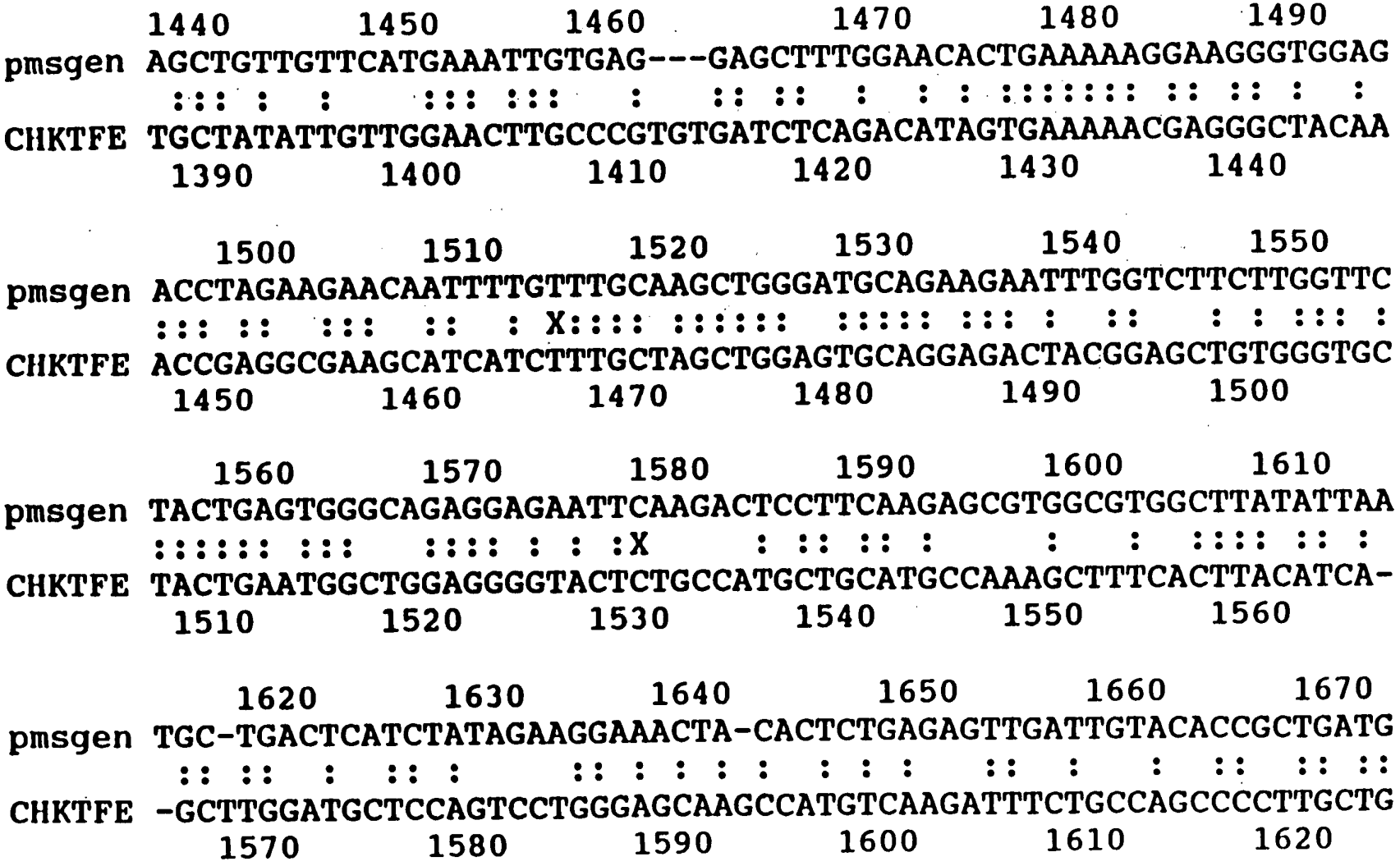

1440 1450 1460 1470 1480 1490
pmsgen AGCTGTTGTTCATGAAATTGTGAG---GAGCTTTGGAACACTGAAAAAGGAAGGGTGGAG
CHKTFE TGCTATATTGTTGGAACTTGCCCGTGTGATCTCAGACATAGTGAAAAACGAGGGCTACAA
1390 1400 1410 1420 1430 1440
1500 1510 1520 1530 1540 1550
pmsgen ACCTAGAAGAACAATTTTGTTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTC
CHKTFE ACCGAGGCGAAGCATCATCTTTGCTAGCTGGAGTGCAGGAGACTACGGAGCTGTGGGTGC
1450 1460 1470 1480 1490 1500
1560 1570 1580 1590 1600 1610
pmsgen TACTGAGTGGGCAGAGGAGAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAA
CHKTFE TACTGAATGGCTGGAGGGGTACTCTGCCATGCTGCATGCCAAAGCTTTCACTTACATCA-
1510 1520 1530 1540 1550 1560
1620 1630 1640 1650 1660 1670
pmsgen TGC-TGACTCATCTATAGAAGGAAACTA-CACTCTGAGAGTTGATTGTACACCGCTGATG
CHKTFE -GCTTGGATGCTCCAGTCCTGGGAGCAAGCCATGTCAAGATTTCTGCCAGCCCCTTGCTG
1570 1580 1590 1600 1610 1620

FIGURE 16-4

```
                1680        1690        1700        1710        1720        1730
pmsgen  TACAGCTTGGTACACAACCTAACAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGC
        :: :    :: :    :  : :: : : :::: :  :: :  : :: ::  ::   ::
CHKTFE  TATATGCTGCTGGGGAGTATTATGAAGGGGGTGAAGAATCCAGCAGGCAGTCTCAGAGAGC
             1630        1640        1650        1660        1670        1680

                1740        1750        1760        1770        1780        1790
pmsgen  AAATCTCTTTATGAAAGTTGGACTAAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCC
          :::: ::   : : :::: : : :
CHKTFE  ----CTCTATAACAGACTTGGCCCCAGACTGGGTAAAGCAGTTGTTCCTCTTGGCCTGGA
                 1690        1700        1710        1720        1730
```

FIGURE 16-5

```
RATTRFR   Rat transferrin receptor mRNA, 3' end.          164   164   311
  55.5% identity in 560 nt overlap

                1210       1220       1230       1240       1250
pmsgen CCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGGCTT-
                                        ::: :: ::: : :  : : :  : : ::
RATTRF TGCAGAAAAGCTATTCAAAAACATGGAAGGAAACTGTCCTCCTAGTTGGAATATAGATTC
     610        620        630        640        650        660

     1260       1270       1280       1290       1300       1310
pmsgen -TACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATC-CACTCT-ACCAATG----
        :  :: :: ::          :: : : :::: :::   : : :::: : : :::::
RATTRF CTCATGTAAGCTGGAACTTTCACAGAATCAAAATGTGAAGCTCACTGTGAACAATGTACT
     670        680        690        700        710        720
```

FIGURE 16-6

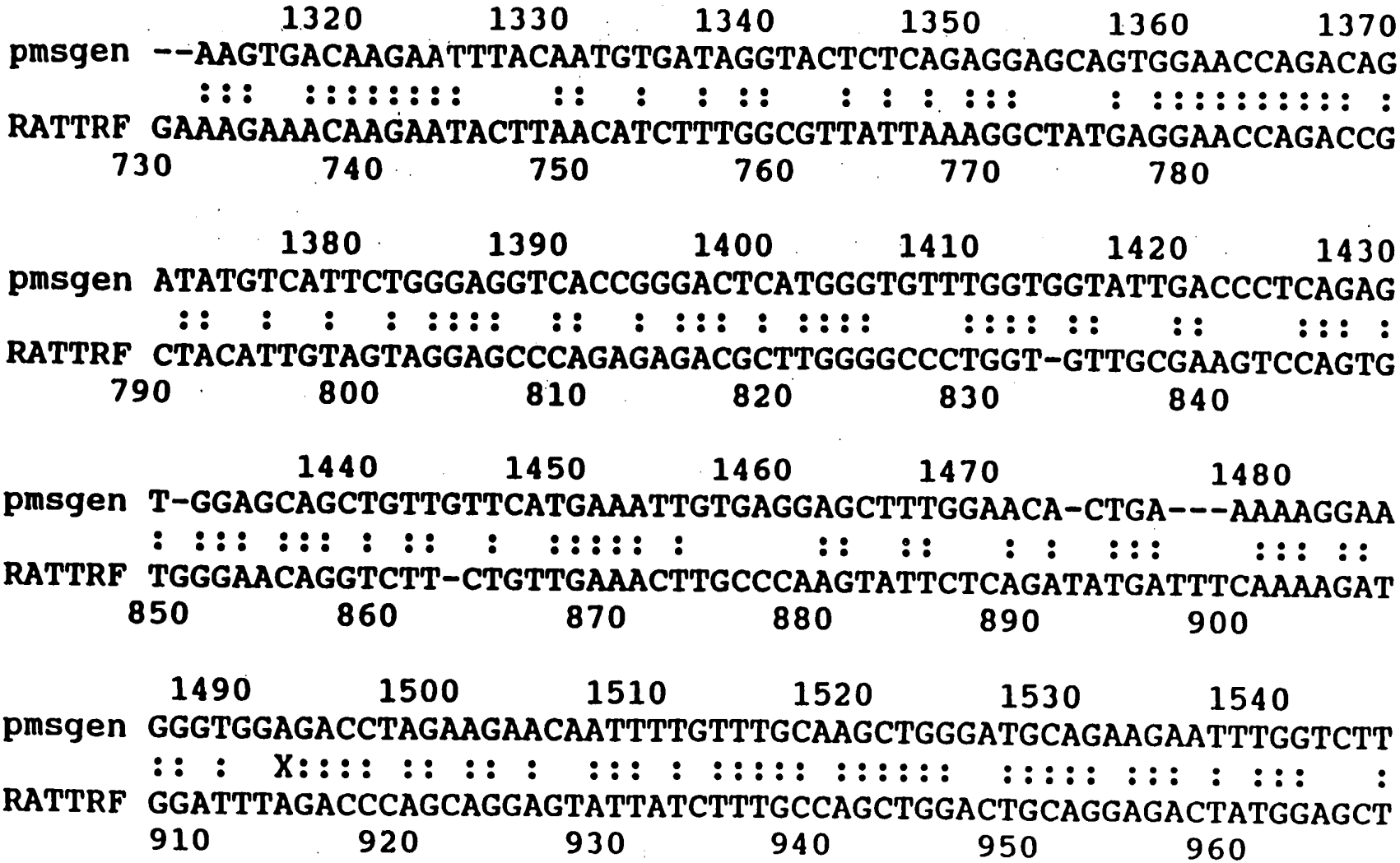


FIGURE 16-7

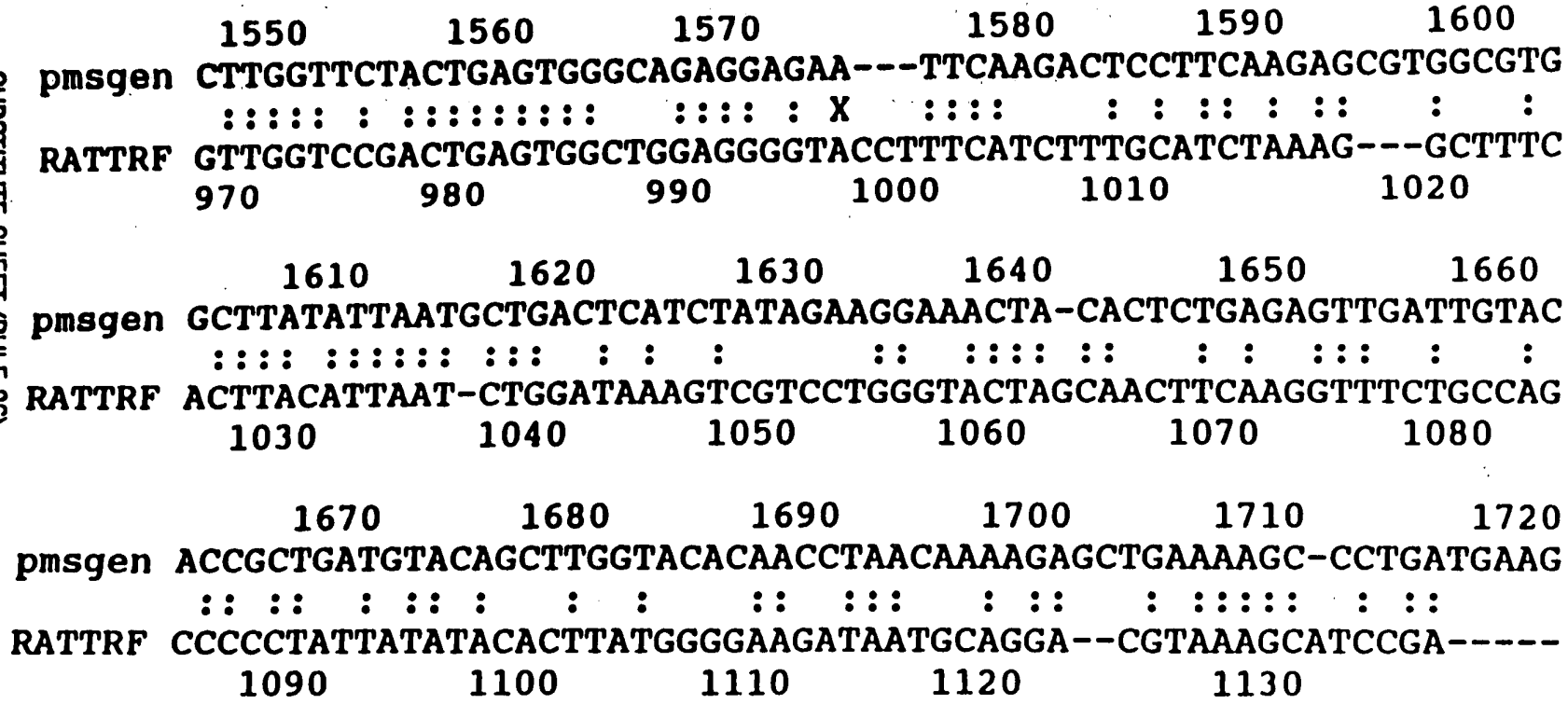


FIGURE 16-8

```
          1730      1740      1750      1760      1770
pmsgen GCTTTGAAGGCAAATCTCTTTAT-GAA-----AGTTGGACTAAAAAAAGTCCTTCCCCAG
       :::: :: :::: ::: ::: :::    : ::::: ::  :::: :
RATTRF ---TTGATGGAAAATATCTATATCGAAACAGTAATTGGATTAGCAAAATTGAGGAACTTT
          1140      1150      1160      1170      1180      1190

          1780      1790      1800      1810      1820      1830
pmsgen AGTTCAGTGGCATGCCCAGGATAAGCAAATTGGGATCTGGAAATGATTTTGAGGTGTTCT
RATTRF CCTTGGACAATGCTGCATTCCCTTTTCTTGCATATTCAGGAATCCCAGCAGTTTCTTCT
          1200      1210      1220      1230      1240      1250
```

FIGURE 16-9

HUMTFRR Human transferrin receptor mRNA, complete cd 145 145 266
54.3% identity in 464 nt overlap

```
             1230       1240       1250       1260       1270
pmsgen AGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGGCTTTAC-TGGAAACTTTTCTACAC
                                              : : : :: ::: :: :   :  :   : :
HUMTFR TATGGAAGGAGACTGTCCCTCTGACTGGAAAACAGACTCTACATGTAGGATGGTAACCTC
     1140       1150       1160       1170       1180       1190

    1280       1290       1300       1310            1320       1330
pmsgen AAAAAGTCAAGATGCACATC-CACTCT-ACCAATG------AAGTGACAAGAATTTACAA
       : ::::  :  :::   : : :::: : : :::::       ::: :: :: ::::   ::
HUMTFR AGAAAGCAAGAATGTGAAGCTCACTGTGAGCAATGTGCTGAAAGAGATAAAAATTCTTAA
     1200       1210       1220       1230       1240       1250

             1340       1350       1360       1370       1380       1390
pmsgen TGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGATATGTCATTCTGGGAGGTCA
         :  : ::   : : : :::    :: ::::::::    :::::  :  : :: :  ::
HUMTFR CATCTTTGGAGTTATTAAAGGCTTTGTAGAACCAGATCACTATGTTGTAGTTGGGGCCCA
     1260       1270       1280       1290       1300       1310

             1400       1410       1420       1430       1440       1450
pmsgen CCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGT-GGAGCAGCTGTTGTTCATG
         : ::  ::::::    ::: : :    :  : : : :: ::  :::::  :  :
HUMTFR GAGAGATGCATGGGGCCCTGGAGCTGCAAAATC-CGGTGTAGGCACAGCTCTCCTATTGA
     1320       1330       1340       1350       1360       1370
```

FIGURE 16-10

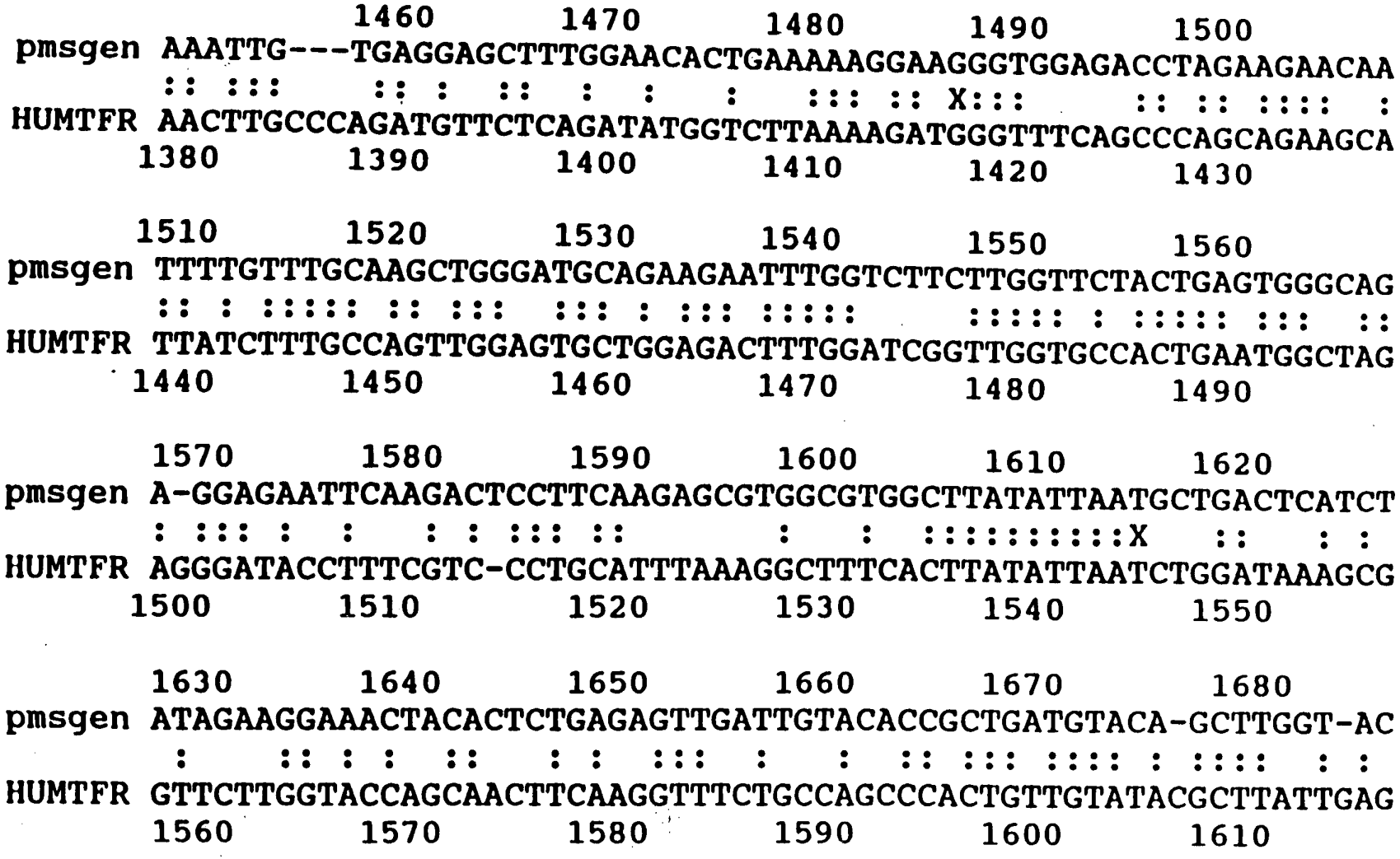


FIGURE 16-11

```
          1690       1700       1710       1720       1730       1740
pmsgen ACAACCTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTTATG
       :  :::   :::::
HUMTFR AAAACAATGCAAAATGTGAAGCATCCGGTTACTGGGCAATTTCTATATCAGGACAGCAAC
          1620       1630       1640       1650       1660       1670
```

FIGURE 17A

FIGURE 17B

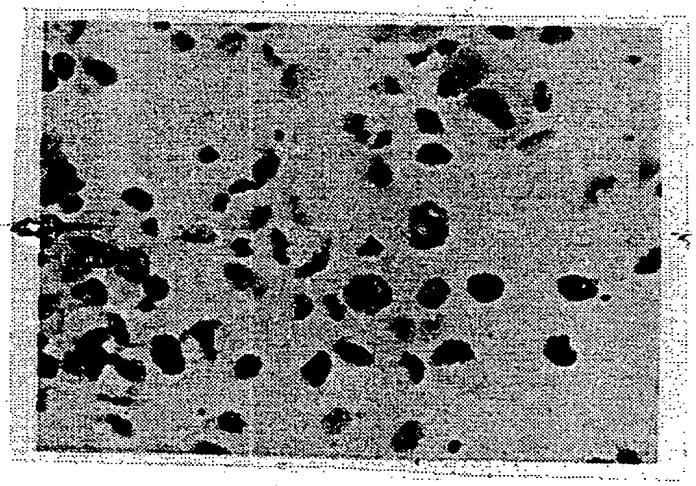


FIGURE 17C

FIGURE 18

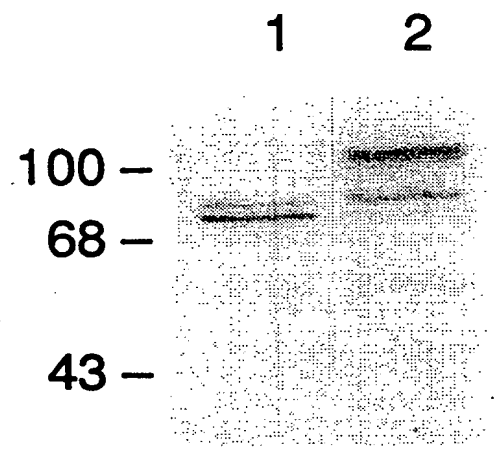


FIGURE 19

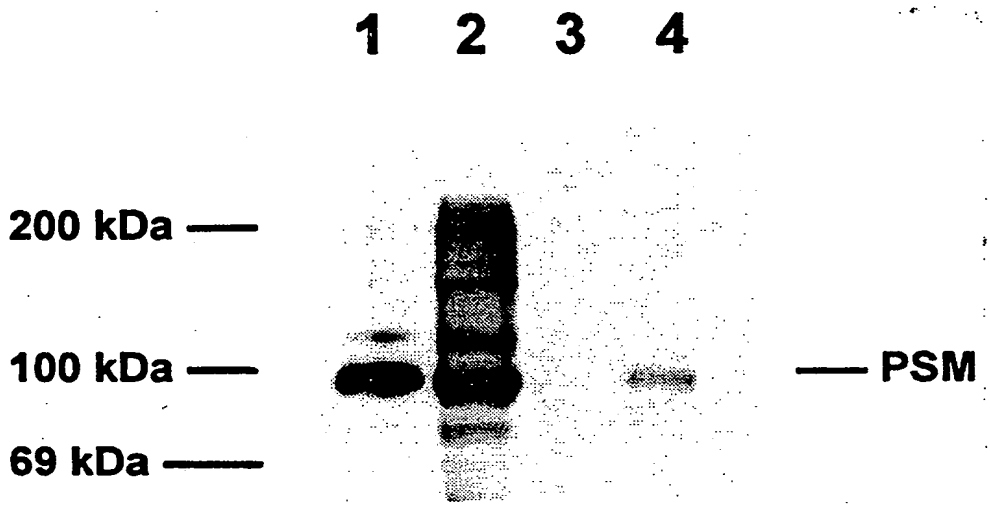


FIGURE 20

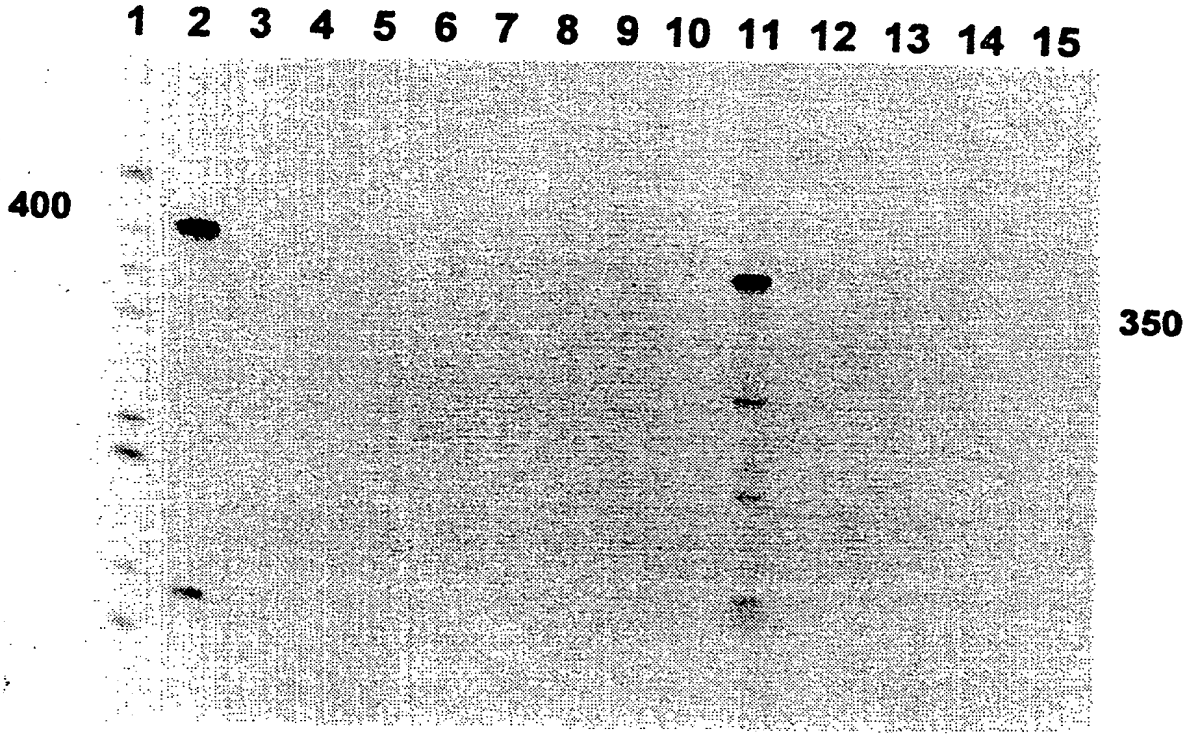


FIGURE 21

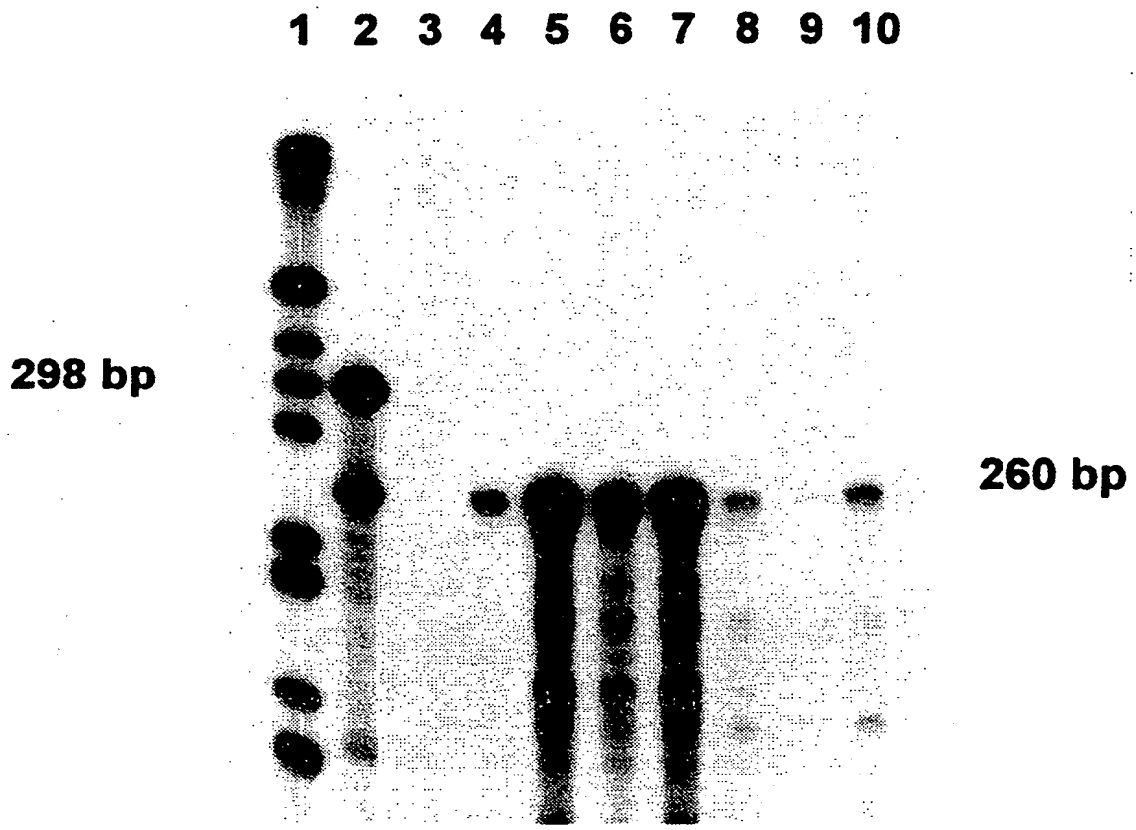


FIGURE 22

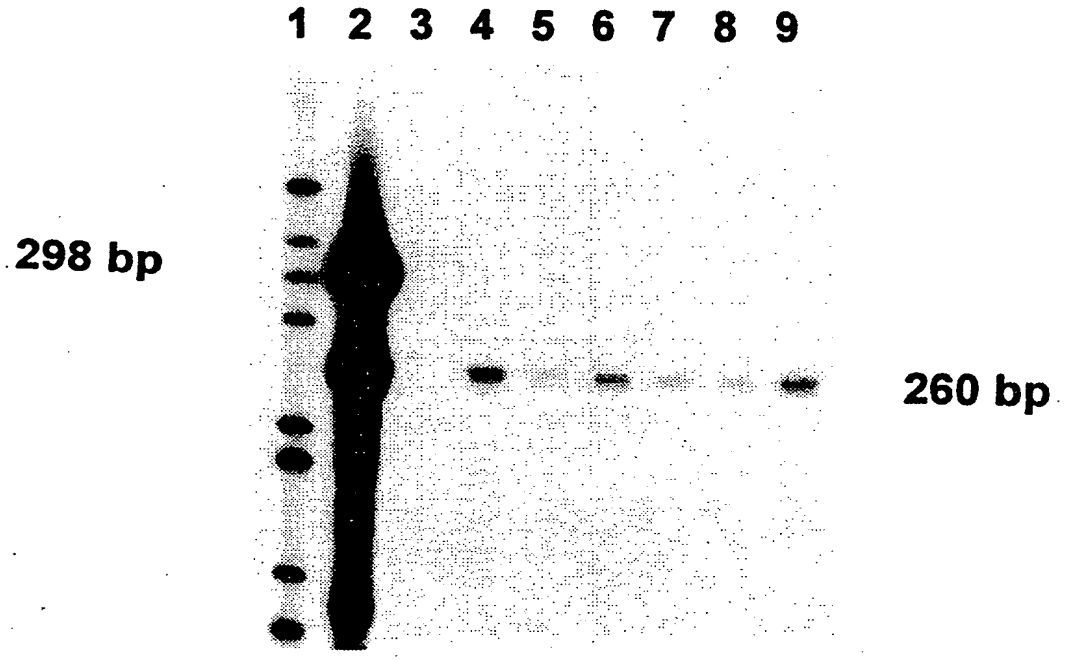


FIGURE 23

CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	–	–
A9(11) (A9+HUM. 11)	YES	NO	–	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES	–	–
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES	–	–
R1564 (RAT MAMMARY)	NO	YES	–	–
R1564-11-c14	YES	YES	–	+
R1564-11-c15	YES	YES	–	REPEAT
R1564-11-c16	YES	YES	–	ND
R1564-11-c12	YES	YES	ND	+

FIGURE 24A

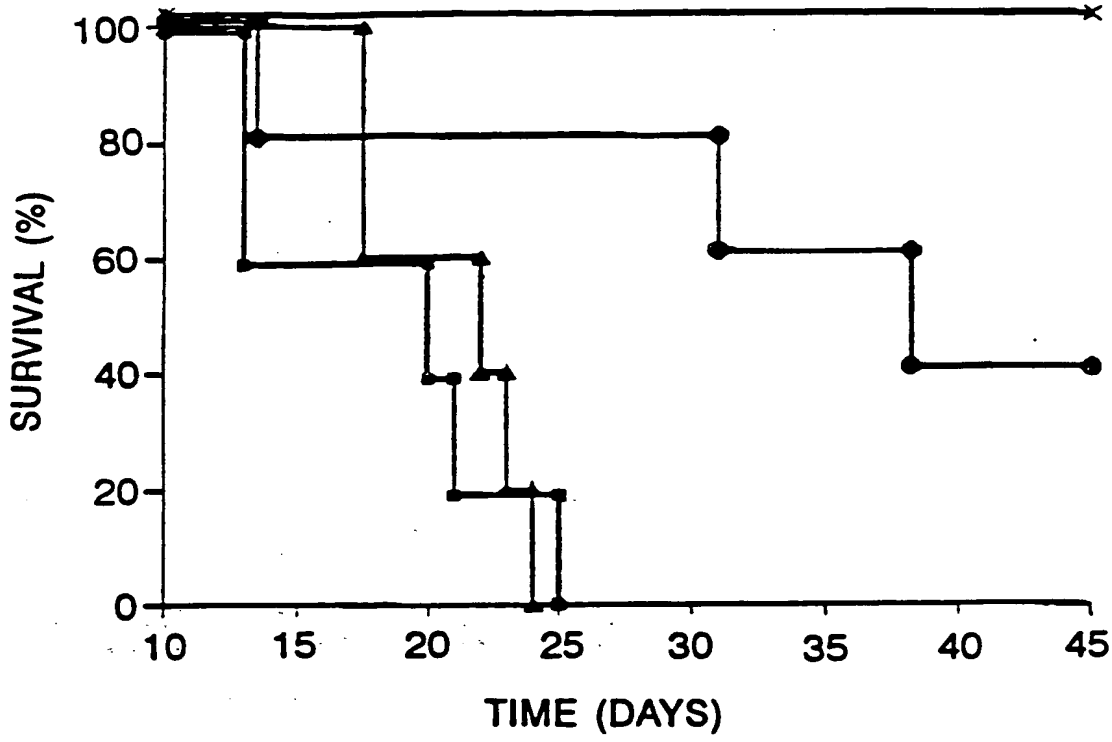


FIGURE 24B

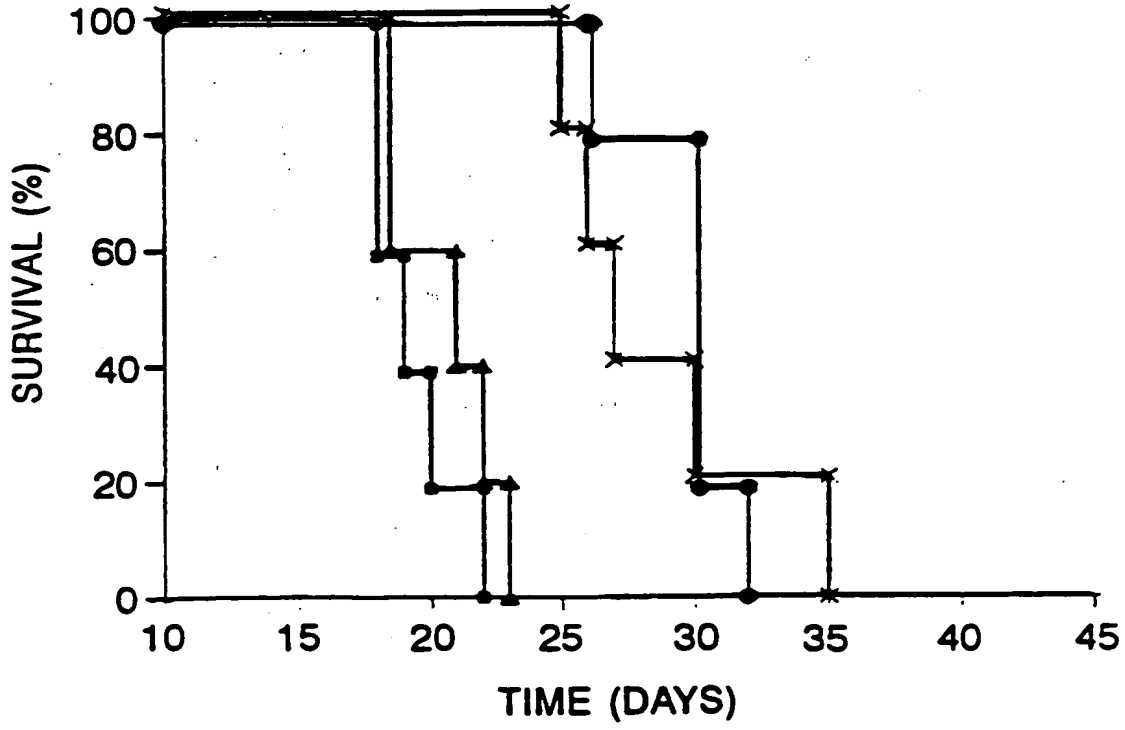


FIGURE 25A

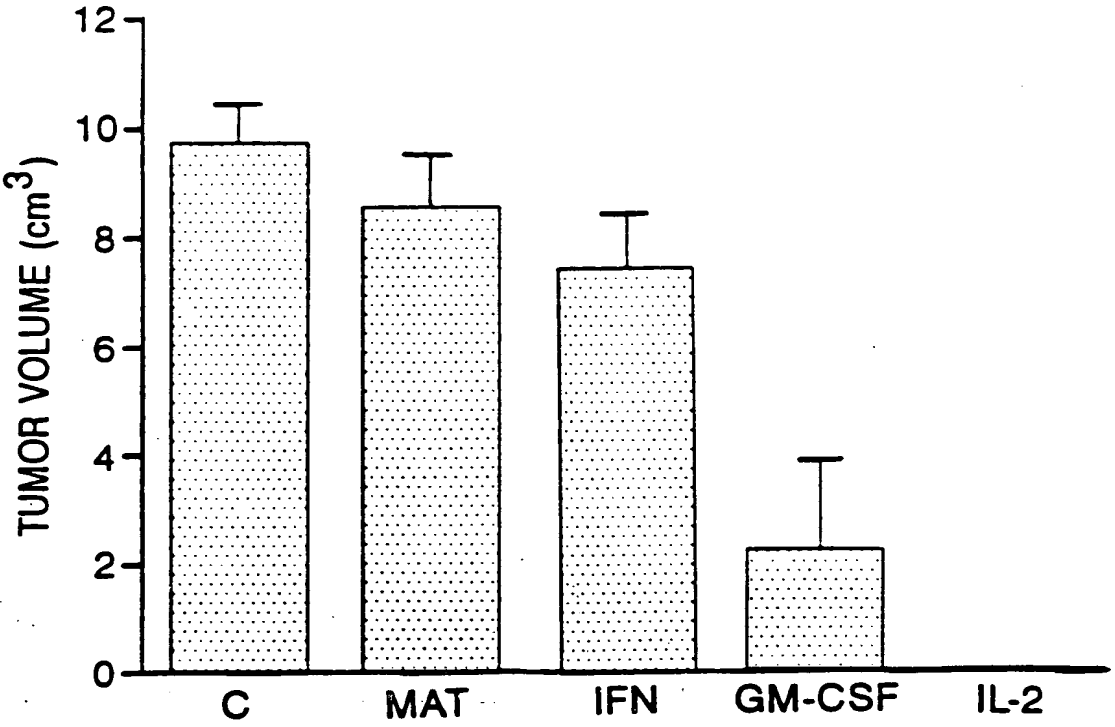


FIGURE 25B

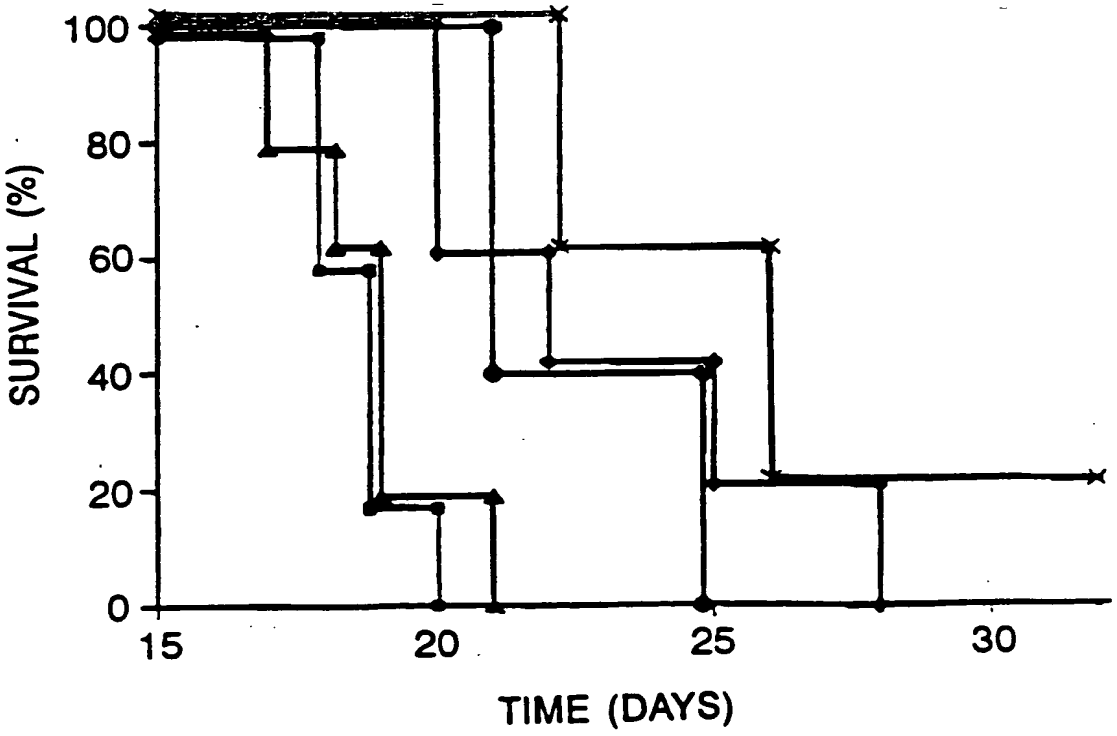


FIGURE 26

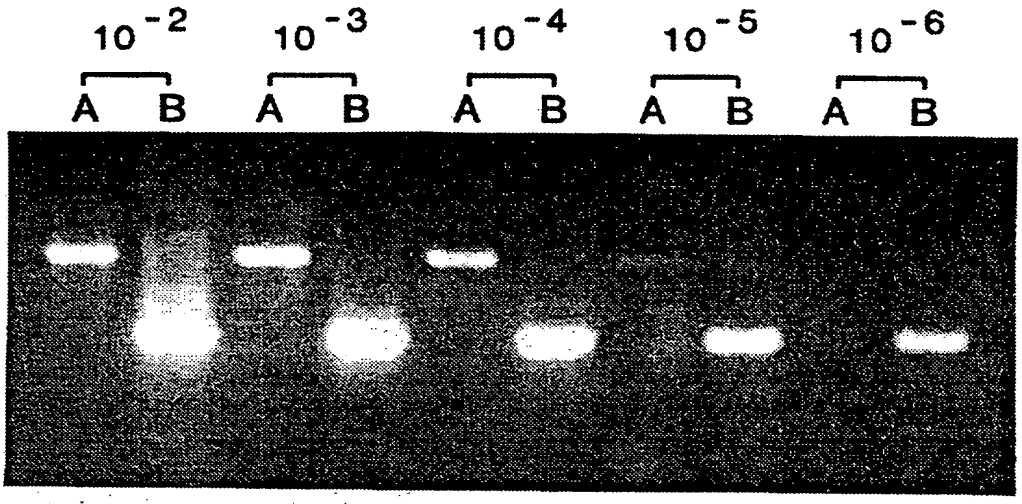


FIGURE 27

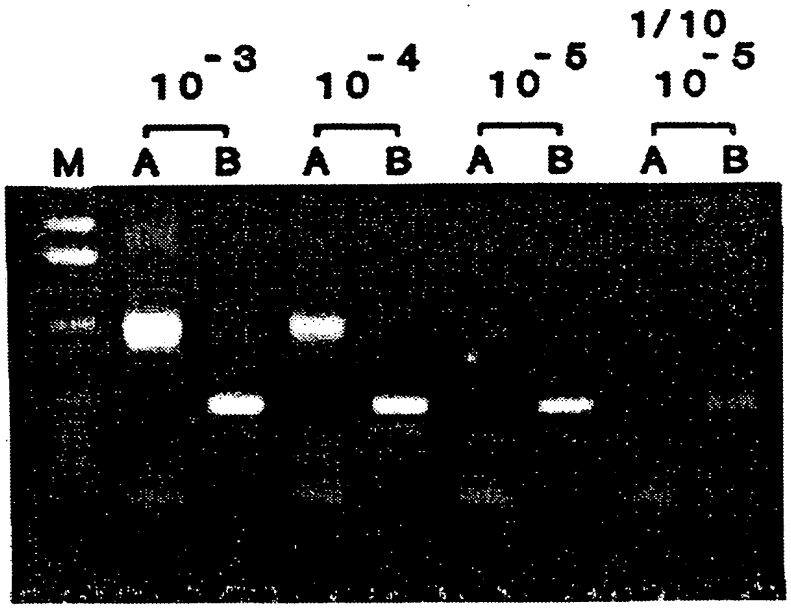


FIGURE 28

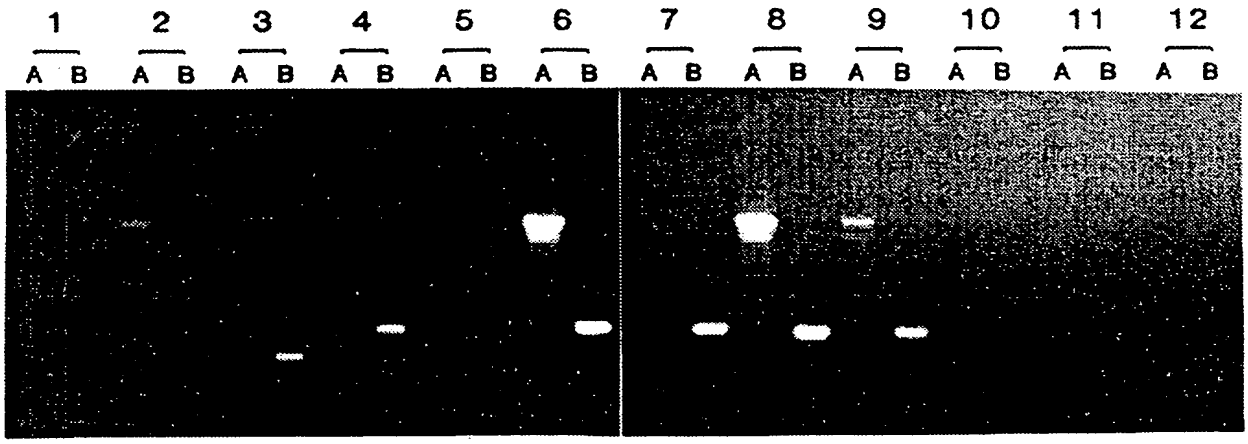
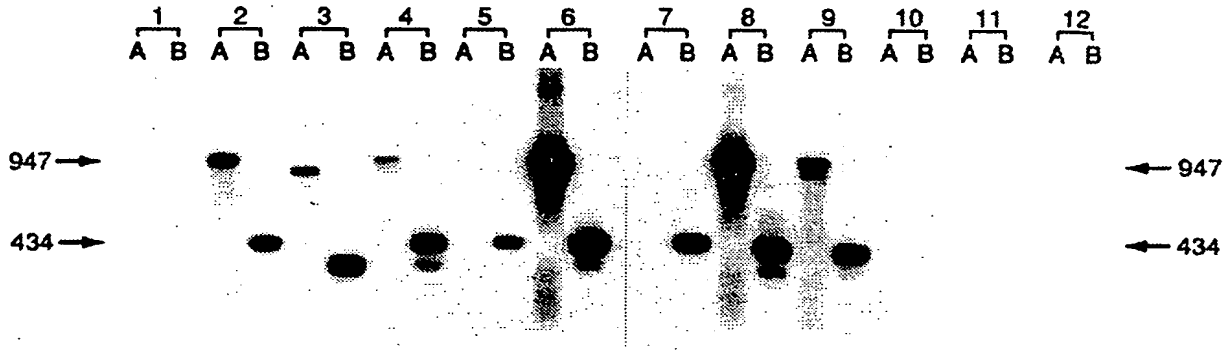


FIGURE 29


1 2 3 4 5 6 7 8 9 10 11 12
A B A B A B A B A B A B A B A B A B A B A B A B
947
434
947
434

08/466381

FIGURE 30

Patient	Stage	Treatment	PSA	PAP	PSA-PCR	PSM-PCR
1	T2NxMo	None	8.9	0.7	–	+
2	T2NoMo	RRP 7/93	6.1	–	–	+
3	T2CNoMo	PLND 5/93	4.5	0.1	–	+
4	T2BNoMo	RRP 3/92	NMA	0.4	–	+
5	T3NxMo	Proscar + Flutamide	51.3	1.0	–	+
6	Recur T3	I-125 1986	54.7	1.4	–	+
7	T3ANoMo	RRP 10/92	NMA	0.3	–	+
8	T3NxMo	XRT 1987	7.5	0.1	–	–
9	T3NxMo	Proscar + Flutamide	35.4	0.7	–	–
10	D2	S/P XRT Flutamide +Emcyt	311	4.5	+	+
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+
12	T2NoMo	RRP 8/91	NMA	0.5	–	+
13	T3NoMo	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	–	–
14	D1	PLND 1989 XRT 1989	1.6	0.4	–	–
15	D1	Proscar + Flutamide	20.8	0.5	–	–
16	T2CNoMo	RRP 4/92	0.1	0.3	–	–